

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new subfamily, *Santaclaravirinae* with three genera (Class *Caudoviricetes*). |
| **Code assigned:** | 2025.071B.Santaclaravirinae\_1nsf\_3ng\_6ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Andrew M. | Kropinski | Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada | Phage.Canada@gmail.com | x |
| Cristina | Moraru | Carl von Ossietzky Universität Oldenburg, Germany | liliana.cristina.moraru@uol.de |  |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **x** |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| Caudoviricetes Study Group |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 15/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:** |
| *Brief description of current situation:*  *Proposed changes:*  *Justification:* |

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| **Text of General Proposal:** |
| *Background:*  *Proposed* *changes:*  *Justification:* |

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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

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**Part 3:** **TAXONOMIC PROPOSAL**

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **x** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *Santaclaravirinae* | Named in honour of Santa Clara University where two of the Escherichia phages were identified |
| *Cyranovirus* | Named after Escherichia phage Cyrano |
| *Suquintavirus* | Named after Salmonella phage SSU5 |
| *Westmeadvirus* | Names after The Westmead Institute for Medical Research, where Klebsiella phage pJN2-26 was isolated |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: subfamily, genus and species  *Description of current taxonomy*: Phage-plasmids are a novel, hybrid class of mobile genetic element which retain aspects of both phages and plasmids. These genetic elements have not been previously classified by ICTV.  *Proposed* *taxonomic change(s):* Create a new subfamily, “*Santaclaravirinae”* with three genera “*Cyranovirus”, “Westmeadvirus”* and “*Suquintavirus”*  *Justification*: This proposal is in accord with our definition of a subfamily |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: subfamily, genus and species  *Description of current taxonomy*: Phage-plasmids are a novel, hybrid class of mobile genetic element which retain aspects of both phages and plasmids. These genetic elements have not being previously classified by ICTV.  *Proposed* *taxonomic change(s):* Create a new subfamily, “*Santaclaravirinae”* with three genera “*Cyranovirus”, “Westmeadvirus”* and “*Suquintavirus”*  *Demarcation criteria:* The Bacterial and Archaeal Virus Subcommittee established 70% average nucleotide identity (ANI) threshold for genus classification or 95% ANI for species [8]. Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny [8].  *Justification*: This proposal is in accord with our definition of a subfamily |

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| **References:** |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870  2. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.  3. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/  4. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287. https://www.genome.jp/viptree/  5. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. PubMed PMID: 12142423  6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.  7. Davis P, Seto D, Mahadevan P. CoreGenes5.0: An Updated User-Friendly Webserver for the Determination of Core Genes from Sets of Viral and Bacterial Genomes. Viruses. 2022 Nov 16;14(11):2534. doi: 10.3390/v14112534. PMID: 36423143; PMCID: PMC9693508.  8. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.  Lemoine F, Correia D, Lefort V, Doppelt-Azeroual O, Mareuil F, Cohen-Boulakia S, Gascuel O. NGPhylogeny.fr: new generation phylogenetic services for non-specialists. Nucleic Acids Res. 2019 Jul 2;47(W1):W260-W265. doi: 10.1093/nar/gkz303. PMID: 31028399; PMCID: PMC6602494.  9. Letunic I, Bork P. Interactive Tree Of Life (iTOL): an online tool for phylogenetic tree display and annotation. Bioinformatics. 2007 Jan 1;23(1):127-8. doi: 10.1093/bioinformatics/btl529. Epub 2006 Oct 18. PMID: 17050570.  10. Zhou T, Xu K, Zhao F, Liu W, Li L, Hua Z, Zhou X. itol.toolkit accelerates working with iTOL (Interactive Tree of Life) by an automated generation of annotation files. Bioinformatics. 2023 Jun 1;39(6):btad339. doi: 10.1093/bioinformatics/btad339. PMID: 37225402; PMCID: PMC10243930. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

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**Figure 1.** VIRIDIC heat map of a group of phages with the one under discussion. VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in **black** correspond to strains. Abbreviations: Kleb = *Klebsiella*; Salm = *Salmonella*; Esch = *Escherichia*; phg = phage.

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**Figure 2.** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages belonging to this subfamily are indicated with **red bar**.

**Table 1.** Characteristics of new species in the genus *Westmeadvirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Klebsiella* phage pJN2-26 | *Klebsiella pneumoniae* ST4656 isolate JN2-26 | Siphovirus | Temperate | MZ779062.1 | 109952 bp | 129 | 1 |

(a) Possesses chromosome (plasmid) partitioning proteins ParA and ParB together with integrase; (b) *Klebsiella* phages GArcari-2022a and vB\_Kpn\_1825-KPC53 have not been annotated; (c) *Klebsiella* phage T13-OXA48phi12.3 is significantly smaller than any of the other phages in this genus

**Table 2.** Characteristics of species in the genus *Suquintavirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Salmonella* phage SSU5 | *Salmonella enterica* subsp. *enterica* serovar Typhimurium strain LT2 | Siphovirus | Temperate | JQ965645.1 | 103,229 bp | 130 | 1 |

**Specific reference:** Kim M, Kim S, Ryu S. Complete genome sequence of bacteriophage SSU5 specific for *Salmonella enterica* serovar Typhimurium rough strains. J Virol. 2012 Oct;86(19):10894. doi: 10.1128/JVI.01796-12. PMID: 22966187; PMCID: PMC3457314.

Points: (a) SSU5 showed a high level of sequence identity to cryptic plasmid pHCM2 (106,516 bp; NC\_003385) harbored by *Salmonella* Typhi strain CT18

**Points:** (a) possesses ParA/B and lysis/lysogeny switch proteins

**Table 3.** Characteristics of species in the genus *Cyranovirus*

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| **Phage name** | **Host** | **Morphotype** | **Lifestyle** | **Accession No.** | **Genome size** | **No. proteins** | **No. tRNA** |
| *Escherichia* phage Cyrano | *Escherichia coli* LF82 | Siphovirus | Temperate | OV696614.1 | 108379 bp | 123 | 3 |
| Escherichia phage CMS-2020a | *Escherichia coli* strain SCU-175 | Siphovirus | Temperate | CP054387.2 | 109272 bp | 168 | 3 |
| Escherichia phage CMS-2020b | *Escherichia coli* strain SCU-107 | Siphovirus | Temperate | CP053388.2 | 107648 bp | 172 | 3 |

**Points:** (a) possesses ParA/B and lysis/lysogeny switch proteins

**CoreGenes 3.5 Analysis [7]**: revealed that the phages listed above share 83 protein homologs terminase large subunit, major capsid protein, Ig-like domain-containing protein, tail tape measure protein, minor tail protein related to those of coliphage Lambda, holin, endolysin, two spannins, ParA/ParB family protein, DNA primase, DNA helicase, DNA ligase, cobalamin biosynthesis protein CobT, DNA polymerase III alpha subunit, DNA polymerase I, RecA-like recombinase, Cre associated protein, exonuclease, two ribonucleotide-diphosphate reductases, thymidylate synthase, dihydrofolate reductase, adenine methyltransferase, ribonuclease H, and ABC transporter. This indicates that approximately 65.4% of the phage-encoded proteins are conserved.